

SEQUENCE LISTING

<110> UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.

<120> DNA SEQUENCE AND EXPRESSED RECOMBINANT GLYCOPROTEINS
RELATED TO FELINE THYROTROPIN

<130> 235-00540201

<140> PCT/US04/03779

<141> 2004-11-12

<150> 60/534,205

<151> 2004-01-05

<150> 60/519,302

<151> 2003-11-12

<160> 18

<170> PatentIn Ver. 3.3

<210> 1

<211> 118

<212> PRT

<213> Felis sp.

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Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys Tyr Ala Leu Ser
35 40 45

Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys Thr Val Glu Ile
50 55 60

Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser Tyr Pro Val Ala
65 70 75 80

Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr Ser Asp Cys Ile
85 90 95

His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro Gln Lys Ser Asp
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Val Val Gly Val Ser Ile
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<212> PRT

<213> Felis sp.

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 35 40 45
 Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50 55 60
 Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
 65 70 75 80
 Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85 90 95
 Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
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 Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
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 Gln Lys Ser Asp Val Val Gly Val Ser Ile
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 35 40 45
 Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu Ala Thr Cys Cys
 50 55 60
 Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly Asn Ala Lys Val
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 85 90 95

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 35 40 45

 Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala
 50 55 60

 Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
 65 70 75 80

 Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
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 Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys
 100 105 110

 Ser Thr Cys Tyr His His Lys Ile
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      20           25           30

Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys Tyr Ala Leu Ser
      35           40           45

Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys Thr Val Glu Ile
      50           55           60

Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser Tyr Pro Val Ala
      65           70           75           80

Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr Ser Asp Cys Ile
      85           90           95

His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro Gln Lys Ser Asp
      100          105          110

Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser Lys Ala Pro Ser
      115          120          125

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Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro Ser Asp Thr Pro
 130 135 140

Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro
 145 150 155 160

Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro
 165 170 175

Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 180 185 190

Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu
 195 200 205

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Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr Cys Tyr
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His His Lys Ile

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<213> Felis sp.

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Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
 35 40 45

Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50 55 60

Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
 65 70 75 80

Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85 90 95

Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
 100 105 110

Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
 115 120 125

Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
 130 135 140

Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro
 145 150 155 160

Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met
 165 170 175

Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys
 180 185 190

Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala
 195 200 205

Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
 210 215 220

Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
 225 230 235 240

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 245 250 255

Ser Thr Cys Tyr His His Lys Ile
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caa gcg atg tct ttt tgt ttt cca act gag tat atg atg cat gtc gaa 96
 Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
 20 25 30

agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc tgt gct 144
 Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
 35 40 45

gga tat tgt atg aca cgg gat atc aat ggc aaa ctg ttt ctt ccc aaa 192
 Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50 55 60

tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag 240
 Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
 65 70 75 80

act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc 288
 Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85 90 95

tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act gac tat 336
 Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
 100 105 110

agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc aaa ccc 384
 Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
 115 120 125

cag aag tcc gat gtg gta gga gtt tct atc taa 417
 Gln Lys Ser Asp Val Val Gly Val Ser Ile
 130 135

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 accatcaaca ccaccatctg tgctggatat tggatgacac gggatgttag ttcatctcac 180
 ttcttttagc tggaaattag ataaacctag actcagtccaa ttctatccaa gaaaggaaat 240
 gagataaatac acaacacctat ttccacagacc taacggcat tggctccctaa gaggttagatg 300
 cccttagtta taatatacgg acctactccaa tacagttggat acagataatt ttacaatag 360
 ttttactccc aaagtttatt taaaacctat cttgttccca cgtcaagga taaaagagag 420
 gtgtgtgtgt atgtcatttt tttttgtctc tataggattc agtgtggata tgctgaattt 480
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 gcgaattaac atttgtcttc ctcttcgtt ctccctca gatataatg gcaaaactgtt 600
 tcitccaaa tatgctctgt cccaaagatgt ttgcacctac agagacttcc tgcataagac 660
 ttagaaata ccaggatgcc cacaccatgt tactccctat ttctccatcc cggttagctgt 720
 aagctgtaaa tggcaagt gtaatactga ctatagcgac tgcatacatg aggccatcaa 780
 gacaaatgtatgtacccaaac cccagaagtc cgatgtggta ggagttctaa tctaa 835

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 aaggaaaaca aatacttctc caagttgggt gcccccaattt atcaatgcat gggctgctgc 180
 ttctccagag cataccacac tccagcaagg tccaagaaga caatgttgggt cccaaagaac 240
 atcacccatcg aagccacatg ctgtgtggcc aaagccttta ccaaggccac ggtaatggga 300
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<212> DNA
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<222> (100)..(459)
<223> coding region for SEQ ID NO: 4

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ctgatcacat cctgcaaaaaa gtccggagga aggagagcc atg gat tac tac aga      114
                                         Met Asp Tyr Tyr Arg
                                         1                   5

aaa tat gca gct gtc att ctg gcc ata ctc tct gtg ttt ctg cat att      162
Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser Val Phe Leu His Ile
10          15          20

ctc cat tct ttt cct gat gga gag ttt aca atg cag ggg tgc cca gaa      210
Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro Glu
25          30          35

tgc aag cta aag gaa aac aaa tac ttc tcc aag ttg ggt gcc cca att      258
Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro Ile
40          45          50

tat caa tgc atg ggc tgc tgc ttc tcc aga gca tac ccc act cca gca      306
Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Ala
55          60          65

agg tcc aag aag aca atg ttg gtc cca aag aac atc acc tca gaa gcc      354
Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu Ala
70          75          80          85

aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc acg gta atg gga aat      402
Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly Asn
90          95          100

gcc aaa gtg gag aat cac aca gag tgc cac tgc agc act tgc tat cac      450
Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr Cys Tyr His
105         110         115

cac aag att
His Lys Ile
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<211> 792
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<223> coding region for SEQ ID NO: 5

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caa gcg atg tct ttt tgt ttt cca act gag tat atg atg cat gtc gaa 96
Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
 20          25          30

agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc tgt gct 144
Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
 35          40          45

gga tat tgt atg aca cgg gat atc aat ggc aaa ctg ttt ctt ccc aaa 192
Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50          55          60

tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag 240
Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
 65          70          75          80

act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc 288
Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85          90          95

tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act gac tat 336
Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
100          105          110

agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc aaa ccc 384
Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
115          120          125

cag aag tcc gat gtg gta gga gtt tct atc cag gac tcc tct tcc tca 432
Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
130          135          140

aag gcc cct tcc gcc agc ctt cca agc cca acg cgt ctc ccg ggg ccc 480
Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro
145          150          155          160

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tcg gac acc ccg atc ctc cca caa ttt cct gat gga gag ttt aca atg	528
Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met	
165	170
175	
cag ggg tgc cca gaa tgc aag cta aag gaa aac aaa tac ttc tcc aag	576
Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys	
180	185
190	
ttg ggt gcc cca att tat caa tgc atg ggc tgc tgc ttc tcc aga gca	624
Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala	
195	200
205	
tac ccc act cca gca agg tcc aag aag aca atg ttg gtc cca aag aac	672
Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn	
210	215
220	
atc acc tca gaa gcc aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc	720
Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala	
225	230
235	240
acg gta atg gga aat gcc aaa gtg gag aat cac aca gag tgc cac tgc	768
Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys	
245	250
255	
agc act tgc tat cac cac aag att	792
Ser Thr Cys Tyr His His Lys Ile	
260	

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accatcaaca ccaccatctg tgctggatat tttatgcac gggatgttag ttcatctcac 180
ttcttttagc tggaaaattag ataaacctag actcagtcctt tttctatccat gaaaggaaat 240
gagataaattt acaacaccttcat ttcacagacc taacggtcat tggctccat gaggttagagt 300
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gcgaattaac attttgcattt ctcttcgtt cttccctcag gatataatg gcaaaactgtt 600
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tgttagaaata ccaggatgcc cacaccatgt tactccctat ttctccatcc cggtagctgt 720
aagctgtaaa tttggcaagt gtaataactga ctatagcgac tgcatacatg aggccatcaa 780
gacaaatgtt ttgtacccaaac cccagaatgtt cgtatgtgtt ggagttctt tccaggactc 840
ctcttcctca aaggccccctt ccggccagcc tccaaagccca acgcgtctcc cggggccctc 900
ggacaccccg atccctccac aatttccatgat tggagatgtt acaatgcagg ggtgcccaga 960
atgcaagctt aaggaaaaca aatacttctc caagttgggtt gcccccaattt atcaatgcatt 1020
gggctgtgc ttctccagag cataccccac tccagcaagg tccaaagaaga caatgttgggt 1080
cccaaaagaac atcacctcag aagccacatg ctgtgtggcc aaagccttta ccaaggccac 1140
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ccacaagattt 1210

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 tgatggagag 130

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 tctcacttct ttagctgaa aattagataa acctagactc agtccatttc tatccagaaa 240
 gaaaaatgaga taaatcacaa cctcatttca cagacctaacc ggtcattggc tccttagagg 300
 tagagttccct agtttataat atacggaccc actccataaca gttggtagacag ataattttta 360
 caatagttt actcccaaag tttattttaa ccttataatgg ttcccacgat caaggataaaa 420
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 caagactgtt gaaataccag gatgccaca ccatgttact ccctatttct cctaccgggt 720
 agctgttaagc tggaaatgtg gcaagtgtaa tactgactat agcgactgca tacatgaggc 780
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 Met Asp
 1

tac tac aga aaa tat gca gct gtc att ctg gcc ata ctc tct gtg ttt 165
 Tyr Tyr Arg Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser Val Phe
 5 10 15

ctg cat att ctc cat tct ttt cct gat gga gag ttt aca atg cag ggg 213
 Leu His Ile Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met Gln Gly
 20 25 30

tgc cca gaa tgc aag cta aag gaa aac aaa tac ttc tcc aag ttg ggt	261
Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly	
35 40 45 50	
gcc cca att tat caa tgc atg ggc tgc tgc ttc tcc aga gca tac ccc	309
Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro	
55 60 65	
act cca gca agg tcc aag aag aca atg ttg gtc cca aag aac atc acc	357
Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr	
70 75 80	
tca gaa gcc aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc acg gta	405
Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val	
85 90 95	
atg gga aat gcc aaa gtg gag aat cac aca gag tgc cac tgc agc act	453
Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr	
100 105 110	
tgc tat cac cac aag att atc gaa ggt cgt gac tac aag gac gat gac	501
Cys Tyr His His Lys Ile Ile Glu Gly Arg Asp Tyr Lys Asp Asp Asp	
115 120 125 130	
gat aag taagcggccg ctatg	522
Asp Lys	
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Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser	
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Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys	
35 40 45	
Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala	
50 55 60	
Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn	
65 70 75 80	
Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala	
85 90 95	
Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys	
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115 120 125	

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<222> (7)..(168)

<220>
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Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala
1 5 10

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tgt gga caa gcg atg tct ttt tgt ttt cca act gag tat atg atg cat 96
Cys Gly Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His
15          20          25          30

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gtc gaa agg aaa gag tgt gct tat tgc cta acc atc aac acc acc acc atc      144
Val Glu Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile
          35           40           45
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tgt gct gga tat tgt atg aca cgg gtatgttagtt catctcactt cttttagctg 198
Cys Ala Gly Tyr Cys Met Thr Arg
50

aaaatttagat aaacctagac tcagtcatt tctatccaga aaqgaaatqa qataaatcac 258

aacacctt cattt cacagaccta acggtcattq qctccttaqa qqttaqaqtcc ctaqqttata 318

atatacggac ctactccata cagtggatc aqataattt tacaataqtt ttactcccaa 378

agtttatata aaccttatct tgttcccacq atcaaqqata aaaqaqaqqt qtqtqtqtat 438

qqqactaaqq aatcctcccc caqtccatt tqtatctataq qqatqtaaqc qaattaacat 558

tttgccttccct cttctgtgct tcccttcag gat atc aat ggc aaa ctg ttt ctt 610
Asp Ile Asn Gly Lys Leu Phe Leu

ccc aaa tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg 658
Pro Lys Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu

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tac aag act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat 706
Tyr Lys Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr
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Ser Ser Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro		
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Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
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Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
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Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
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Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
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Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
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Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
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Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro
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Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met
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Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys
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Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala
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Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
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Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
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Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys
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Ser Thr Cys Tyr His His Lys Ile Ile Glu Gly Arg Asp Tyr Lys Asp
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Asp Asp Asp Lys
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